

SEQUENCE LISTING

<110> Bruce, Wesley B.

<120> A Nitrate-Responsive Root  
Transcriptional Factor

<130> 1263

<150> US 60/238,292

<151> 2000-10-05

<160> 2

<170> FastSEQ for Windows Version 3.0

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<211> 1280

<212> DNA

<213> Zea mays

<220>

<221> CDS

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tcctcccttg ggaaacctgc tgccttttag ctttcttctt cgagagctcc caccagatct		180
cctccctccctt accttctttg gcacggttcgg cggcgccgcgg gggaaaagat agatcccccc		240
atcgtcgatcg tcgggtccttg ctccgatcg gagggccaca accacaacct ctgcgtccat		300
agcgtgcaag cgccgagccag ggtcaagaag agagctagct agctataaggc cggagatcg		359
atg ggg agg gga aag atc gtg atc cgc agg atc gat aac tcc acg acg		407
Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser		
1 5 10 15		

cggtt cag gtgtt acc ttttcc aag cgc cgg aac ggg atc ttc aag aag gcc	455
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala	
20 25 30	

aat gag ctc gcc atc ctc tgc gat gtc gag gtc ggc ctc gtc atc ttc	503
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe	
35 40 45	

tcc agc acc ggc cgc ctc tac gag tac tct agc acc agc atg aaa tca	551
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser	
50 55 60	

gtt ata gat cgg tac ggc aag gcc aag gaa gag cag caa gtc gtc gca	599
Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala	
65 70 75 80	

aat ccc aac tcg gag ctt aag ttt tgg caa agg gag gca gca agc ttg	647
Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu	
85 90 95	

TOMCAT 4.2502660

aga caa caa ctg cac aac ttg caa gaa aat tat cgg cag ttg acg gga Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly 100	105	110	695	
gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag tcc ctg gag aat Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn 115	120	125	743	
caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag aag gac cat ctc Gln Leu Glu Thr Ser Leu Arg Gly Val Ala Lys Lys Asp His Leu 130	135	140	791	
ttg ata gat gag att cac gat ttg aat cga aag gca agt tta ttt cac Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His 145	150	155	160	839
caa gaa aat aca gac ttg tac aat aag atc aac ctg att cgc caa gaa Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu 165	170	175	887	
aat gat gag tta cat aaa aag ata tat gag act gaa gga cca agt gga Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly 180	185	190	935	
gtt aat cgg gag tca ccg act cca ttc aac ttt gca gta gta gaa acc Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr 195	200	205	983	
aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca cag caa aat Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn 210	215	220	1031	
aac att gag cca tct act gct cct aag cta gga ttg caa tta att cca Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro 225	230	235	240	1079
tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact atttattgtg *				1132
aagagatgat actcagagaa agacatattt gtggcagggaa gatttgagat atgaacttat aaatgtaatg caaataattt tcagaccgga atgggtcggt ggaattcaga ggatgattgc tttctaaaaa aaaaaaaaaa aaaaaaaaaa				1192 1252 1280
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Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala 20 25 30				
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe 35 40 45				
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser				

50                    55                    60

Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala  
65                    70                    75                    80

Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu  
85                    90                    95

Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly  
100                    105                    110

Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn  
115                    120                    125

Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu  
130                    135                    140

Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His  
145                    150                    155                    160

Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu  
165                    170                    175

Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly  
180                    185                    190

Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr  
195                    200                    205

Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn  
210                    215                    220

Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro  
225                    230                    235                    240

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